

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using SW model

Run on: March 26, 2003, 11:15:29 ; Search time 1171 Seconds
(without alignments)
30.445 Million cell updates/sec

Title: US-10-086-184-2

Perfect score: 21
Sequence: 1 gtcctactgacagatgacac 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_escba:*
2: em_escba:*
3: em_escba:*
4: em_escba:*
5: em_escba:*
6: em_escba:*
7: em_escba:*
8: em_escba:*
9: gb_esc1:*
10: gb_esc2:*
11: gb_esc3:*
12: gb_esc3:*
13: gb_esc4:*
14: gb_esc5:*
15: em_escfun:*
16: em_escfun:*
17: gb_esc6:*
18: em_esc6:*
19: em_esc6:*
20: em_esc6:*
21: em_esc6:*
22: em_esc6:*
23: em_esc6:*
24: em_esc6:*
25: em_esc6:*
26: em_esc6:*
27: em_esc6:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.2	58.1	35	17	AZ819702 2M0091A01
2	12	57.1	39	17	BH792327
3	11.8	56.2	30	17	AZ780490
4	11.6	55.2	33	17	DR190235
5	11.6	55.2	34	17	BH812254
6	11.6	55.2	37	17	AZ465387

7	11.4	54.3	29	17	AZ794355
8	11.4	54.3	37	17	AZ507623
9	11.4	54.3	38	17	AZ783438
10	11.4	54.3	38	17	BH789778
11	11.4	54.3	39	17	BH855660
12	11.2	53.3	37	9	AA444863
13	11.2	53.3	37	17	BH850593
14	11	52.4	22	17	AZ496170
15	11	52.4	31	14	R68337
16	11	52.4	37	17	AO073641
17	11	52.4	40	17	AZ436389
18	11	52.4	40	17	BH759445
19	10.8	51.4	22	17	TA235A05Q
20	10.8	51.4	22	17	TA334H05Q
21	10.8	51.4	27	17	AZ439712
22	10.8	51.4	27	17	TA130G05P
23	10.8	51.4	32	13	BJ065561
24	10.6	50.5	32	17	AZ407990
25	10.6	50.5	34	17	AO025206
26	10.6	50.5	36	17	TA119B10Q
27	10.6	50.5	37	9	AA877091
28	10.6	50.5	37	17	AZ458505
29	10.6	50.5	40	17	BH800126
30	10.4	49.5	22	17	AZ806828
31	10.4	49.5	26	17	AZ619253
32	10.4	49.5	26	17	TA120A05P
33	10.4	49.5	31	17	AZ856886
34	10.4	49.5	33	17	AZ451738
35	10.4	49.5	33	17	AZ481982
36	10.4	49.5	35	17	BH811059
37	10.4	49.5	35	17	BH851755
38	10.4	49.5	38	10	AV969052
39	10.4	49.5	39	12	BE874819
40	10.4	49.5	40	9	AI023350
41	10.4	49.5	40	9	AI666981
42	10.2	48.6	26	17	TA336D06Q
43	10.2	48.6	27	17	BH791867
44	10.2	48.6	30	17	AZ941284
45	10.2	48.6	31	9	AI016099

ALIGNMENTS

RESULT 1
LOCUS AZ819702 35 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0091A01R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0091A01 R, DNA sequence.
ACCESSION AZ819702
VERSION AZ819702.1 GI:12989610
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 35)
REFERENCE Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

9 a 10 c 3 g 8 t

ORIGIN

Query Match

Best Local Similarity 56.2%; Score 11.8; DB 17; Length 30;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5 TACTGATAGAGTGA 19

Db 18 TACAATAGAGTGA 4

RESULT 4

DR190235

LOCUS

DEFINITION Danio rerio genomic clone Dkey-19023, genomic survey sequence.

ACCESSION

AL743211

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1.33

/db_xref="taxon:7955"

/clone="Dkey-19023"

/release_type="Testis"

/note="Vector pindigobAC-536"

BASE COUNT

10 a 6 c 7 g 10 t

ORIGIN

Query Match

Best Local Similarity 77.8%; Score 11.6; DB 17; Length 33;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 TCTCTAGTATAGAGTGA 19

Db 10 TCTCTAGTATAGAGTGA 27

RESULT 5

BH812254/c

LOCUS

DEFINITION

34 bp DNA linear GSS 02-MAY-2002

BH812254

LOCUS

DEFINITION

34 bp DNA linear GSS 02-MAY-2002

BH812254

LOCUS

DEFINITION

34 bp DNA linear GSS 02-MAY-2002

ACCESSION

BH812254

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1.34

/db_xref="taxon:3702"

/clone="SALK_061508"

/note="PCR was performed on Arabidopsis thaliana lines"

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tDNA_protocols.html

BASE COUNT

9 a 11 c 5 g 9 t

ORIGIN

Query Match

Best Local Similarity 77.8%; Score 11.6; DB 17; Length 34;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 GCTACTGATAGAGTGA 20

Db 18 GCGCTGAGAGAGATAC 1

RESULT 6

AZ465387

LOCUS

DEFINITION

1M0275113F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0275113 F, DNA sequence.

ACCESSION

VERSION

KEYWORDS

ORGANISM

SOURCE

house mouse

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

1 (bases 1 to 37)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: 1 column: 13
Seq primer: CGTTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 37.
Location/Qualifiers

FEATURES
source

1..37
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0275113"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

9 a 1 c 19 g 8 t

Query Match 55.2%; Score 11.6; DB 17; Length 37;
Best Local Similarity 77.8%; Pred. No. 7.3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GTGCTACTGATGAGTGT 18
Db 19 GGCTACTGTAGAGAGT 36

RESULT 7
AZ794355 29 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0048A11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0048A11 F, DNA sequence.
ACCESSION AZ794355
VERSION AZ794355.1 GI:12940238
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0048 row: A column: 11
Seq primer: CGTTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers

FEATURES
source

1..29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0048A11"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

5 a 7 c 10 g 7 t

Query Match 54.3%; Score 11.4; DB 17; Length 29;
Best Local Similarity 71.4%; Pred. No. 8.2e+04;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GTGCTACTGATGAGTGTACC 21
Db 7 GTGGCATGATGATGATGAC 27

RESULT 8
AZ507623 37 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0349A20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0349A20 F, DNA sequence.
ACCESSION AZ507623
VERSION AZ507623.1 GI:1068939
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0349 row: A column: 20
Seq primer: CGTTGTAAACGACGCCAGCT
Class: plasmid ends
High quality sequence stop: 37.

FEATURES

source

1. .37
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0349A20"
/clone_11b="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

4 a 2 c 12 g 19 t

ORIGIN

Query Match 54.3%; Score 11.4; DB 17; Length 37;
Best Local Similarity 71.4%; Pred. No. 9.2e+04;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GTGCTACTGATAGTGATACC 21
Db 2 GTGTTGTGTTGAGTGATAC 22

RESULT 9
A2783438 38 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0025H12F Mouse 10kb plasmid U08C1M library Mus musculus genomic
DEFINITION clone U08C1M0025H12 F, DNA sequence.
ACCESSION A2783438
VERSION A2783438.1 GI:12918166
KEYWORDS GSS.
SOURCE Mus musculus
ORGANISM house mouse.
Mammalia; Euteleostomi; Chordata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 38)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0025 row: H column: 12
Seq primer: CGTTGTAAACGACGCCAGCT
Class: plasmid ends
High quality sequence stop: 38.

FEATURES

source

1. .38
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C2M0025H12"
/clone_11b="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

10 a 10 c 11 g 7 t

ORIGIN

Query Match 54.3%; Score 11.4; DB 17; Length 38;
Best Local Similarity 71.4%; Pred. No. 9.3e+04;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GTGCTACTGATAGTGATACC 21
Db 1 GTGCTAAGGTGAGAGAAATAC 21

RESULT 10
BH789778 38 bp DNA linear GSS 02-APR-2002
LOCUS SALK_046680.48.35.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_046680.48.35.x, DNA sequence.
ACCESSION BH789778
VERSION BH789778.1 GI:19882876
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 38)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadgilnab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmermann, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker


```

BASE COUNT      8 a      14 c      8 g      7 t
ORIGIN
Query Match      53.3%; Score 11.2; DB 9; Length 37;
Best Local Similarity 81.2%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 ACTGATAGAGTGTACC 21
      ||| ||| ||| ||| |||
      ||| ||| ||| ||| |||
Db      29 ACTGTGAGAGTGTGCC 14

RESULT 13
BH850593      37 bp      DNA      linear      GSS 13-JUN-2002
LOCUS      SALK_071553.14.35.x Arabidopsis thaliana TDNA insertion lines
DEFINITION      Arabidopsis thaliana genomic clone SALK_071553.14.35.x, DNA
sequence.
ACCESSION      BH850593
VERSION      BH850593
KEYWORDS      GSS.
SOURCE      chae crees.
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
REFERENCE      1 (bases 1 to 37)
AUTHORS      Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadinb
,C., Jeske,A., Karnes,M., Kim,C.U., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J., and Ecker,J.R.
TITLE      A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL      Unpublished (2001)
COMMENT      Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
FEATURES
source
Classes: TDNA tagged.
Location/Qualifiers
1..37
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_071553.14.35.x"
/note="PCR was performed on Arabidopsis thaliana lines"
/clone_1ib="Arabidopsis thaliana TDNA insertion lines"
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html."

BASE COUNT      16 a      2 c      10 g      9 t
ORIGIN
Query Match      53.3%; Score 11.2; DB 17; Length 37;
Best Local Similarity 81.2%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 ACTGATAGAGTGTACC 21
      ||| ||| ||| ||| |||
      ||| ||| ||| ||| |||
Db      22 AGTGATAGAGTGTACC 37

RESULT 14
AZ496170      22 bp      DNA      linear      GSS 05-OCT-2000
LOCUS      1M0332N13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0332N13 F, DNA sequence.

```

```

ACCESSION      AZ496170
VERSION      AZ496170.1 GI:10671985
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 22)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhuesern,A.,
and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0332 row: N column: 13
Seq primer: CGTTGTAACGACGCGCAGT
Classes: plasmid ends
High quality sequence stop: 22.
FEATURES
source
Location/Qualifiers
1..22
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0332N13"
/clone_1ib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g114732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT      7 a      4 c      5 g      6 t
ORIGIN
Query Match      52.4%; Score 11; DB 17; Length 22;
Best Local Similarity 73.7%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TGCTACTGATAGAGTGTAC 20
      ||| ||| ||| ||| |||
      ||| ||| ||| ||| |||
Db      1 TGATATAATGAGCTGTAC 19

RESULT 15
R68337/c      31 bp      mRNA      linear      EST 01-JUN-1995
LOCUS      Y106h02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:138483 5' similar to SP:S33957 S33957; COAT PROTEIN GAMMA-COP

```

- BOVINE ;, mRNA sequence.

ACCESSION R68337
VERSION R68337.1 GI:841854

KEYWORDS EST.

SOURCE

ORGANISM

human.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 31)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maira, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston,
R., Williamson, A., Wohlmann, P., and Wilson, R.
The WashU-Merck EST Project

TITLE

Unpublished (1995)

JOURNAL

Contact: Wilson RK

COMMENT

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1412

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LBNL

This clone is available royalty-free through LBNL; contact the

IMAGE Consortium (info@image.lbnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone; similarity on wrong strand

Insert length: 1412 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

FEATURES

Location/Qualifiers

1..31

/organism="Homo sapiens"

/db_xref="GDB:544867"

/db_xref="taxon:9606"

/clone="IMAGE:138483"

/clone_lib="Soares placenta Nb2HP"

/sex="Female"

/dev_stage="Placenta obtained at birth (full term)"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: Placenta; Vector: pTZ19 (Pharmacia) with a

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I - 01190 (dt) primer (5'

AACTGAGAGATTCCGCGCCGAGAGATTTTCTTTTCTTTT 3'),

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pTZ19 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo. "

BASE COUNT

13 a 9 c 4 g 5 t

ORIGIN

Query Match 52.4%; Score 11; DB 14; Length 31;

Best Local Similarity 73.7%; Pred. No. 1.3e+05;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TGCCTAGTATGAGGTAC 20

DB 22 TGATGTTCTAGAGGTAC 4

Search completed: March 26, 2003, 23:18:00
Job time: 11173 secs